

## SEQUENCE LISTING

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&lt;120&gt; Modified promoters

&lt;130&gt; KS0817

&lt;150&gt; JP 2004-062853

&lt;151&gt; 2004.03.05

&lt;160&gt; 18

&lt;170&gt; PatentIn Ver. 3.1

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&lt;213&gt; Bacillus sp. KSM-S237

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Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile Ala	
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Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu	
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Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu	
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Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro	
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Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp	
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His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala	
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Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly Asn	
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Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val Phe	
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Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro Tyr	
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Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn Ile	
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Gly	Pro	Ser	Ala	Asn	Trp	Val	Asn	Pro	Asn	Arg	Ala	Ile	Lys	Val	Glu	
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Pro	Thr	Asn	Phe	Val	Pro	Leu	Gly	Asp	Lys	Phe	Lys	Ala	Glu	Leu	Thr	
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Glu	Asn	Asn	Asn	Ile	Asn	Asn	Ile	Ile	Leu	Phe	Val	Gly	Thr	Glu	Gly	
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Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu			
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Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys			
675	680	685	
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Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg			
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gtc ttt gta gat aat gtt cgt ttt gag ggg gct gct act act gag ccg			2907
Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro			
725	730	735	
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Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp			
740	745	750	
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Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys			
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gaa gca gta aaa gaa gaa aag aaa gaa gct aaa gaa gaa aag aaa gca			3051
Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala			
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Ala Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly  
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Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val  
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Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro  
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Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn  
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Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly  
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Pro Gly Pro Asp Gln Val Trp Val Pro Glu Glu Leu Ser Leu Ser Gly  
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Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys  
 370 375 380

Gln Gly Phe Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile  
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Glu Asn Glu Ala Gly Ala Leu Lys Leu Ser Gly Leu Asp Ala Ser Asn  
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Asp Val Ser Glu Gly Asn Tyr Trp Ala Asn Ala Arg Leu Ser Ala Asp  
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Asp Val Ile Val Asp Glu Pro Thr Thr Val Ser Ile Ala Ala Ile Pro



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Gly Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu				
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Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro				
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Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu				
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Gly Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg				
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Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr				
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Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp				
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Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val				
	675		680	685

Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu  
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Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly  
705 710 715 720

Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu  
725 730 735

Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val  
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aatgacatc atataaacia atttgtctac caatcactat ttaaagctgt ttatgatata      180
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Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu Asn Asp	
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Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu Ser Asp	
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Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly Asn Ser	
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gtt gct gat tgg ttt aag cca ctt gct tat gcg aca att ttg acg cgt Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu Thr Arg 340 345 350	1336
gaa ggt ggt tat cca aat gta ttt tac ggt gat tac tat ggg att cct Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro 355 360 365 370	1384
aac gat aac att tca gct aaa aaa gat atg att gat gag ctg ctt gat Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu Leu Asp 375 380 385	1432
gca cgt caa aat tac gca tat ggc acg cag cat gac tat ttt gat cat Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe Asp His 390 395 400	1480
tgg gat gtt gta gga tgg act agg gaa gga tct tcc tcc aga cct aat Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Arg Pro Asn 405 410 415	1528
tca ggc ctt gcg act att atg tcg aat gga cct ggt ggt tcc aag tgg Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser Lys Trp 420 425 430	1576
atg tat gta gga cgt cag aat gca gga caa aca tgg aca gat tta act	1624

Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp Leu Thr  
435 440 445 450

ggg aat aac gga gcg tcc gtt aca att aat ggc gat gga tgg ggc gaa 1672  
Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp Gly Glu  
455 460 465

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Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln  
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Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly  
35 40 45

Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu  
50 55 60

Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys  
65 70 75 80

Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn  
85 90 95

Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr  
100 105 110

Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp  
115 120 125

Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser  
130 135 140

Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe  
 145 150 155 160

Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg  
 165 170 175

Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn  
 180 185 190

Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val  
 195 200 205

Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp  
 210 215 220

Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr  
 225 230 235 240

Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu  
 245 250 255

Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe  
 260 265 270

Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu  
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Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met  
 290 295 300

Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala  
 305 310 315 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu  
 325 330 335

Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu  
 340 345 350

Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly  
 355 360 365



Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu  
 370 375 380

Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe  
 385 390 395 400

Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg  
 405 410 415

Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser  
 420 425 430

Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp  
 435 440 445

Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp  
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Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln  
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 <212> DNA  
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